

AMENDMENTS TO THE CLAIMS:

This listing of claims will replace all prior versions and listings of claims in the application:

1. (Currently amended) A method of identifying a test cell, tissue, or nucleus, comprising:

obtaining a DNA methylation pattern for the test cell, tissue, or nucleus, wherein the DNA methylation pattern for the test cell, tissue, or nucleus comprises information on the methylation state of CpG at a plurality of gene regions;

obtaining a cell-, tissue-, or nucleus-specific DNA methylation pattern for one or more known types of cell, tissue, or nucleus; and,

comparing the DNA methylation pattern ~~of~~for the test cell, tissue, or nucleus with the cell-, tissue-, or nucleus-specific DNA methylation pattern~~of the one or more known types of~~, wherein the test cell, tissue, or nucleus is identified if the DNA methylation pattern of the test cell, tissue, or nucleus matches the cell-, tissue-, or nucleus-specific DNA methylation pattern. ~~, thereby identifying the cell, tissue or nucleus.~~

2. (Canceled)

3. (Canceled)

4. (Withdrawn) A computer-readable record medium in which a program that permits a computer to function as an identification system for cells, tissues or nuclei has been recorded, said identification system comprising:

(a) means for analyzing information on the methylation pattern of DNA isolated from a test cell, tissue or nucleus; and

(b) means for identifying the cell, tissue or nucleus using the analysis results as an indicator.

5. (Currently amended) A method of ~~assessing~~identifying the differentiation state of a test cell, tissue, or nucleus comprising:

obtaining a DNA methylation pattern for the test cell, tissue, or nucleus, wherein the DNA methylation pattern for the test cell, tissue, or nucleus comprises information on the methylation state of CpG at a plurality of gene regions;

obtaining a differentiation state-specific DNA methylation pattern for one or more cell, tissue, or nucleus of known differentiation state; and,

comparing the DNA methylation pattern ~~of~~for the test cell, tissue, or nucleus with the differentiation state-specific DNA methylation pattern ~~of the one or more cell, tissue or nucleus of known differentiation state,~~ wherein the differentiation state of the test cell, tissue, or nucleus is identified if the DNA methylation pattern of the test cell, tissue, or nucleus matches the differentiation state-specific DNA methylation pattern thereby ~~assessing the differentiation state of the cell, tissue or nucleus.~~

6. (Currently amended) The method of claim 5, wherein the DNA methylation patterns for the test cell, tissue, or nucleus and the differentiation state-specific DNA methylation pattern each comprise information on the methylation state of at least about 1,000 gene regions.

7. (Currently amended) The method of claim ~~5~~17 or claim 18, further comprising ~~identifying the methylated and demethylated~~determining nucleotide sequence information for differentially methylated gene regions that specify the differentiation state of the test cell, tissue, or nucleus.

8. (Currently amended) The method of claim ~~5~~, wherein the test cell, tissue, or nucleus is a stem cell.

9. (Currently amended) The method of claim 5, wherein the DNA methylation patterns are ~~analyzed~~obtained by generating RLGS profiles.

10. (Currently amended) The method of claim 1, wherein the DNA methylation patterns for the test cell, tissue, or nucleus and the cell-, tissue-, or nucleus-specific DNA methylation pattern each comprise information on the methylation state of at least about 1,000 gene regions.

11. (Currently amended) The method of claim ~~15~~or claim 16, further comprising ~~identifying the methylated and demethylated~~determining nucleotide sequence information for differentially methylated gene regions that specify the identity of the test cell, tissue, or nucleus.

12. (Currently amended) The method of claim 1, wherein the test cell, tissue, or nucleus is a stem cell.

13. (Currently amended) The method of claim 1, wherein the DNA methylation patterns are ~~analyzed~~obtained by generating RLGS profiles.

14. (Withdrawn) A method of producing a differentiated cell, tissue, or nucleus comprising:

methylation or demethylation of the gene regions identified by the method of claim 7 in a cell, tissue, or nucleus, so as to specify a desired differentiation state; and

producing a differentiated cell, tissue, or nucleus.

15. (New) The method of claim 1, wherein obtaining the cell-, tissue-, or nucleus-specific DNA methylation pattern comprises:

obtaining a DNA methylation pattern for one or more known type of cell, tissue, or nucleus, wherein the DNA methylation pattern comprises information on the methylation state of CpG at a plurality of gene regions; and,

identifying gene regions that are differentially and specifically methylated for the known type of cell, tissue, or nucleus.

16. (New) The method of claim 15, wherein obtaining the cell-, tissue-, or nucleus-specific DNA methylation pattern further comprises:

comparing the DNA methylation patterns for more than one known type of cell, tissue, or nucleus; and,

determining the methylation state of CpG at the differentially methylated gene regions for at least one of the more than one known type of cell, tissue, or nucleus, thereby obtaining a cell-, tissue-, or nucleus-specific DNA methylation pattern.

17. (New) The method of claim 5, wherein obtaining the differentiation state-specific DNA methylation pattern comprises:

obtaining a DNA methylation pattern for one or more cell, tissue, or nucleus of known differentiation state, wherein the DNA methylation pattern comprises information on the methylation state of CpG at a plurality of gene regions; and, identifying gene regions that are differentially and specifically methylated for the cell, tissue, or nucleus of known differentiation state.

18. (New) The method of claim 17, wherein obtaining the differentiation state-specific DNA methylation pattern further comprises:

comparing the DNA methylation patterns for more than one cell, tissue, or nucleus of known differentiation state; and,

determining the methylation state of CpG at the differentially methylated gene regions for at least one of the more than one type of cell, tissue, or nucleus of known differentiation state, thereby obtaining a differentiation state-specific DNA methylation pattern.